



PCT10

RAW SEQUENCE LISTING

DATE: 11/18/2002

PATENT APPLICATION: US/10/030,194

TIME: 15:02:28

Input Set : A:\EP.txt

Output Set: N:\CRF4\11182002\J030194.raw

7 <110> APPLICANT: RENARD, MICHEL
 10 DELOURME, REGINE
 13 BARRET, PIERRE
 16 BRUNEL, DOMINIQUE
 19 FROGER, NICOLE
 22 TANGUY, XAVIER
 28 <120> TITLE OF INVENTION: MUTANT GENE OF THE GRAS FAMILY AND PLANTS WITH REDUCED
 29 DEVELOPMENT CONTAINING SAID MUTANT GENE
 35 <130> FILE REFERENCE: 218874US0PCT
 41 <140> CURRENT APPLICATION NUMBER: 10/030,194
 44 <141> CURRENT FILING DATE: 2002-02-04
 50 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02216
 53 <151> PRIOR FILING DATE: 2000-08-02
 59 <150> PRIOR APPLICATION NUMBER: FR 9910023
 62 <151> PRIOR FILING DATE: 1999-08-02
 E--> 68 <160> NUMBER OF SEQ ID NOS: ⑥3 see below
 74 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

Does Not Comply
 Corrected Diskette Needed

714 <210> SEQ ID NO: 3
 717 <211> LENGTH: ①779 *last sequence in submitted file*
 720 <212> TYPE: DNA
 723 <213> ORGANISM: Brassica napus
 729 <220> FEATURE:
 732 <221> NAME/KEY: CDS
 735 <222> LOCATION: (60)..(1778) 589 (see p.2)
 738 <223> OTHER INFORMATION:
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 747 caaccagaa caaaaccaga ccgatctgag agattaacta tatcttaacc agatcagaa 59
 751 atg aag agg gat ctt cat cag ttc caa ggt ccc aac cac ggg aca tca 107
 753 Met Lys Arg Asp Leu His Gln Phe Gln Gly Pro Asn His Gly Thr Ser
 755 1 5 10 15
 759 atc gcc ggt tct tcc act tct tcc cct gcg gtg ttt ggt aaa gac aag 155
 761 Ile Ala Gly Ser Ser Thr Ser Ser Pro Ala Val Phe Gly Lys Asp Lys
 763 20 25 30
 767 atg atg atg gtc aaa gaa gaa gaa gac gac gag ctt cta gga gtc ttg 203
 769 Met Met Met Val Lys Glu Glu Glu Asp Asp Glu Leu Leu Gly Val Leu
 771 35 40 45
 775 ggt tac aag gtt agg tct tct gag atg gct gag gtt gcg ttg aaa ctc 251
 777 Gly Tyr Lys Val Arg Ser Ser Glu Met Ala Glu Val Ala Leu Lys Leu
 779 50 55 60

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783 gag cag ctt gag acg atg atg ggt aac gct caa gaa gac ggt tta gct      299
785 Glu Gln Leu Glu Thr Met Met Gly Asn Ala Gln Glu Asp Gly Leu Ala
787 65              70              75              80
791 cac ctc gcg acg gat act gtt cat tac aac ccc gct gag ctt tac tcg      347
793 His Leu Ala Thr Asp Thr Val His Tyr Asn Pro Ala Glu Leu Tyr Ser
795              85              90              95
799 tgg ctt gat aac atg ctc acg gag ctt aac cca ccc gct gca acg acc      395
801 Trp Leu Asp Asn Met Leu Thr Glu Leu Asn Pro Pro Ala Ala Thr Thr
803              100              105              110
807 gga tct aac gct ttg aac ccg gag att aat aat aat aat aat aac tcg      443
809 Gly Ser Asn Ala Leu Asn Pro Glu Ile Asn Asn Asn Asn Asn Asn Ser
811              115              120              125
815 ttt ttc acc gga ggc gac ctc aaa gcg att cct gga aac gcg gtt tgt      491
817 Phe Phe Thr Gly Gly Asp Leu Lys Ala Ile Pro Gly Asn Ala Val Cys
819              130              135              140
823 cgc aga tct aat cag ttc gcg ttt gcg gtt gat tcg tcg agt aat aag      539
825 Arg Arg Ser Asn Gln Phe Ala Phe Ala Val Asp Ser Ser Ser Asn Lys
827 145              150              155              160
831 cgt ttg aaa ccg tcc tcg agc cct gat tcg atg gtt aca tct cca tca      587
833 Arg Leu Lys Pro Ser Ser Ser Pro Asp Ser Met Val Thr Ser Pro Ser
E--> 835              165              170

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the
correct
nucleotide
total
195 ← insert

VERIFICATION SUMMARY

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Input Set : A:\EP.txt

Output Set: N:\CRF4\11182002\J030194.raw

L:111 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:104
L:745 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:738
L:835 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:835 M:252 E: No. of Seq. differs, <211> LENGTH:Input:1779 Found:587 SEQ:3
L:68 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (6) Counted (3)